GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: April 8, 2003, 14:33:07 ; Search time 47 Seconds
(without alignments)
1114.750 Million cell updates/sec

Title: US-09-001-737-8
Perfect score: 545
Sequence: 1 MAKEIKFSADARAAMVRGVD.....TPAPAMPAGMDPGMMGGMGG 545

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 8

Total number of hits satisfying chosen parameters: 191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	70	12.8	540	2	G95222	chaperonin, 60 kDa
2	70	12.8	540	2	H98086	chaperonin GroEL [
3	56	10.3	542	2	B86674	60 KD chaperonin [
4	31	5.7	542	2	AD1333	class I heat-shock
5	27	5.0	544	2	B36917	heat shock protein
6	27	5.0	544	2	S23918	groEL protein - Ag
7	27	5.0	544	2	B97442	60K chaperonin (pr
8	27	5.0	544	2	AD2660	60 KDA chaperonin
9	27	5.0	545	2	JN0509	heat shock protein
10	27	5.0	545	2	S47530	chaperonin groEL -
11	27	5.0	545	2	C95311	groEL2 chaperonin
12	27	5.0	547	2	I40331	Cpn60 protein (Gro
13	26	4.8	538	2	C89994	GroEL protein [imp
14	26	4.8	539	2	JN0601	heat shock protein
15	26	4.8	541	2	JN0512	heat shock protein
16	26	4.8	542	2	F95967	probable heat shoc
17	26	4.8	542	2	AC1704	class I heat-shock
18	25	4.6	539	2	B49855	heat shock protein
19	25	4.6	541	2	S68249	chaperonin groEL h
20	25	4.6	542	2	JN0661	heat shock protein
21	25	4.6	542	2	S32106	groEL protein - La
22	25	4.6	544	2	JC5130	heat shock protein
23	25	4.6	544	2	JC6063	chaperonin groEL -
24	25	4.6	544	2	B83720	class I heat-shock
25	24	4.4	538	2	JQ1195	heat shock protein
26	24	4.4	544	2	A71555	probable hsp-60 -
27	24	4.4	544	2	B41884	58K heat shock pro
28	24	4.4	544	2	S19023	chaperonin groEL -
29	24	4.4	544	2	I40731	heat shock protein
30	24	4.4	544	2	JL0117	hypB protein - Chl
31	24	4.4	544	2	B41479	60K heat shock pro
32	24	4.4	544	2	F86507	heat shock protein
33	24	4.4	544	2	B81556	60 kDa chaperonin
34	24	4.4	544	2	D81709	60 kDa chaperonin
35	24	4.4	544	2	AG2263	chaperonin GroEL [
36	24	4.4	545	2	G81328	60 kD chaperonin (
37	24	4.4	546	2	I40342	heat shock protein
38	24	4.4	546	2	S22347	groEL - Brucella a
39	23	4.2	543	2	B41872	heat shock protein
40	23	4.2	543	2	F97232	chaperonin GroEL,
41	23	4.2	544	2	S70667	chaperonin groEL -
42	23	4.2	545	2	S51563	heat shock protein
43	23	4.2	546	2	B47073	chaperonin GroEL -
44	23	4.2	547	2	B43606	heat shock protein
45	23	4.2	547	2	B87334	chaperonin, 60 kDa
46	23	4.2	547	2	B83098	GroEL protein PA43
47	22	4.0	544	1	B43827	chaperonin groEL -
48	22	4.0	546	2	AG3640	60K chaperonin gro
49	22	4.0	549	2	JC2564	heat shock protein
50	22	4.0	585	2	S49253	rubisco binding pr
51	21	3.9	541	2	B44425	chaperonin groEL -
52	21	3.9	541	2	T06829	chaperonin groEL -
53	21	3.9	552	2	S39765	chaperonin 60 - Co
54	20	3.7	540	2	A26950	groEL2 protein - M
55	20	3.7	540	2	A43509	65K antigen mbaA -
56	20	3.7	541	2	S40245	heat shock protein
57	20	3.7	541	2	T44725	chaperonin 60K [im
58	20	3.7	544	2	S37039	groEL protein - Ba
59	20	3.7	546	2	S65596	heat shock protein
60	20	3.7	588	2	A25902	65K antigen - Myco
61	19	3.5	541	2	JN0511	heat shock protein
62	19	3.5	541	2	S72614	chaperonin 60 - Th
63	19	3.5	544	1	BVYCGL	chaperonin groEL -
64	19	3.5	546	2	S34938	heat shock protein
65	19	3.5	546	2	S35311	heat shock cognate
66	19	3.5	550	2	S35309	heat shock protein
67	17	3.1	539	2	F70737	chaperonin groEL1
68	17	3.1	544	2	H95269	GroEL3 chaperonin
69	17	3.1	547	2	F82783	60kDa chaperonin X
70	16	2.9	539	2	S22342	chaperonin HSP60 -
71	16	2.9	540	2	S37566	groEL1 protein - S
72	16	2.9	540	2	C41325	heat shock protein
73	16	2.9	540	2	B41325	heat shock protein
74	16	2.9	541	2	S61301	heat shock protein
75	16	2.9	541	2	T35591	chaperonin cpn60 -
76	16	2.9	543	2	D64243	heat shock protein
77	16	2.9	543	2	S73595	heat shock protein
78	16	2.9	544	2	S61300	heat shock protein
79	16	2.9	544	2	S61302	heat shock protein
80	16	2.9	544	2	S61303	heat shock protein
81	16	2.9	544	2	H81964	chaperonin 60kD su
82	16	2.9	544	2	C81021	chaperonin, 60 kDa
83	15	2.8	530	2	D82412	chaperonin, 60 Kd
84	15	2.8	534	2	S26877	groEL protein - re
85	15	2.8	543	2	JC5771	chaperonin groEL-1
86	15	2.8	544	2	B82048	chaperonin, 60 Kd
87	15	2.8	545	2	H70180	heat shock protein
88	15	2.8	546	2	B54539	heat shock protein
89	15	2.8	547	2	JC4519	heat-shock protein
90	15	2.8	547	2	B49203	heat shock protein
91	15	2.8	548	1	BVECGL	chaperonin groEL -
92	15	2.8	548	2	C64076	chaperonin groEL -
93	15	2.8	548	2	B42281	symbionin symL - p
94	15	2.8	548	2	D91269	chaperonin GroEL [
95	15	2.8	548	2	B84932	60 kD chaperonin [
96	15	2.8	548	2	B86110	hypothetical prote
97	15	2.8	548	2	AG0043	60 kDa chaperonin
98	15	2.8	548	2	AE1045	GroEL protein [imp
99	15	2.8	550	2	S52901	heat shock protein
100	15	2.8	550	2	S26423	heat shock protein
101	15	2.8	550	2	A41468	60K heat shock pro
102	15	2.8	551	2	JC2562	chaperonin groELx

103	15	2.8	569	2	S11035	chaperonin hsp60,
104	15	2.8	573	1	A32800	chaperonin GroEL p
105	15	2.8	573	1	HHRT60	chaperonin groEL p
106	15	2.8	573	1	HHMS60	chaperonin groEL p
107	15	2.8	573	2	A34173	mitochondrial prot
108	14	2.6	435	2	S56644	chaperonin 60 beta
109	14	2.6	528	2	S73270	chaperonin, 60K -
110	14	2.6	528	2	S78278	chaperonin 60 - Od
111	14	2.6	537	2	S25181	heat shock protein
112	14	2.6	538	2	H72367	groEL protein - Th
113	14	2.6	543	2	S70013	chaperonin-like pr
114	14	2.6	548	2	H97820	60K chaperonin [im
115	14	2.6	550	2	A71668	60 kd chaperonin (
116	14	2.6	552	2	S74322	chaperonin groEL-2
117	14	2.6	572	2	JQ0157	heat shock protein
118	14	2.6	574	2	T49325	probable heat-shoc
119	13	2.4	174	2	T07736	probable chaperoni
120	13	2.4	544	2	H71374	chaperonin groEL -
121	13	2.4	546	2	S36237	chaperonin groEL -
122	13	2.4	546	2	B71986	60Kda chaperone -
123	13	2.4	588	2	PW0007	chaperonin 62.5K b
124	13	2.4	595	2	T06412	probable chaperoni
125	13	2.4	599	2	T07733	probable chaperoni
126	13	2.4	600	2	JT0901	chaperonin 60 beta
127	13	2.4	600	2	B96597	Rubisco subunit bi
128	12	2.2	259	2	S56646	chaperonin 60 beta
129	12	2.2	545	2	C70489	GroEL - Aquifex ae
130	12	2.2	548	2	G75499	groEL protein - De
131	12	2.2	550	2	S61297	heat-shock protein
132	12	2.2	555	2	B41492	58K antigen - Rick
133	12	2.2	582	2	S62535	heat shock protein
134	12	2.2	582	2	T43369	heat-shock protein
135	12	2.2	589	2	H90112	CPN60 protein [imp
136	12	2.2	611	2	E86388	probable chaperoni
137	11	2.0	114	2	S05292	65K antigen - Myco
138	11	2.0	114	2	S05293	65K antigen - Myco
139	11	2.0	114	2	S05294	65K antigen - Myco
140	11	2.0	114	2	S05295	65K antigen - Myco
141	11	2.0	186	2	PW0008	chaperonine 60K be
142	11	2.0	545	2	PW0005	chaperonine 60K al
143	11	2.0	560	2	AB2043	chaperonin GroEL [
144	11	2.0	562	2	S61295	heat shock protein
145	11	2.0	583	2	S38642	chaperonin 60 alph
146	11	2.0	586	2	S71235	chaperonin 60 alph
147	10	1.8	16	2	C44896	heat shock protein
148	10	1.8	495	1	HHCSBA	chaperonin groEL -
149	10	1.8	524	2	F84742	mitochondrial chap
150	10	1.8	543	1	HHWTBA	chaperonin groEL a
151	10	1.8	575	2	S29315	chaperonin 60 - cu
152	10	1.8	575	2	S29316	chaperonin 60 - cu
153	10	1.8	576	2	S26583	chaperonin hsp60 -
154	10	1.8	577	2	S26582	chaperonin hsp60 -
155	10	1.8	577	2	S20875	chaperonin hsp60 p
156	10	1.8	577	2	S20876	chaperonin hsp60 p
157	10	1.8	580	2	S56645	chaperonin 60 alph
158	10	1.8	587	2	S38634	chaperonin, mitoch
159	10	1.8	587	2	T06518	chaperonin 60 alph
160	9	1.7	220	2	A75362	hypothetical prote
161	8	1.5	131	2	G82684	hypothetical prote
162	8	1.5	156	2	JT0902	chaperonin 60 beta
163	8	1.5	156	2	A36922	orf1 5'of acvB - A
164	8	1.5	177	2	PS0374	chaperonin 60 beta
165	8	1.5	191	2	G81808	hypothetical prote
166	8	1.5	235	2	D95999	probable iron upta
167	8	1.5	240	2	H71435	hypothetical prote
168	8	1.5	333	2	AB3237	hypothetical prote
169	8	1.5	343	2	A95198	phospho-2-dehydro-
170	8	1.5	343	2	E98064	2-dehydro-3-deoxy-
171	8	1.5	355	2	T38483	hypothetical prote
172	8	1.5	391	2	T44839	probable amino-tra
173	8	1.5	431	2	JS0055	hypothetical 43.7K
174	8	1.5	441	2	S19606	hydrogenase regula
175	8	1.5	441	2	AD0931	transcription regu
176	8	1.5	524	2	D84718	probable glutamyl
177	8	1.5	543	2	S53817	thermosome beta ch
178	8	1.5	545	2	JC4270	hyperthermophilic
179	8	1.5	545	2	B69431	thermosome, subuni
180	8	1.5	545	2	P69529	thermosome, subuni
181	8	1.5	546	2	S61294	heat-shock protein
182	8	1.5	548	2	T43915	chaperonin alpha c
183	8	1.5	549	2	F71219	probable thermophi
184	8	1.5	550	2	F75186	thermosome, chain
185	8	1.5	552	2	H69126	chaperonin - Metha
186	8	1.5	557	2	T47128	heat shock protein
187	8	1.5	656	2	D84359	thermosome subunit
188	8	1.5	700	2	S38426	chaperonin 60 prec
189	8	1.5	851	2	G71435	hypothetical prote
190	8	1.5	1325	2	T01037	hypothetical prote
191	8	1.5	1520	1	TVFFA	protein-tyrosine k

ALIGNMENTS

RESULT 1
G95222
chaperonin, 60 kDa [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: G95222
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapp nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95222
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-540 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75976.1; PID:g14973411; GSPDB:GN00164; TIGR
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1906
C;Superfamily: chaperonin groEL

Query Match 12.8%; Score 70; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.9e-61;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     242 NRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITE 301
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Db     242 NRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITE 301

Qy     302 DLGLELKDAT 311
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Db     302 DLGLELKDAT 311
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RESULT 2
H98086
chaperonin GroEL [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: H98086
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S. e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S. y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H98086
A;Status: preliminary
A;Molecule type: DNA

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A;Residues: 1-540 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00525.1; PID:g15459401; GSPDB:GN00174
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL

  Query Match            12.8%;  Score 70;  DB 2;  Length 540;
  Best Local Similarity  100.0%;  Pred. No. 5.9e-61;
  Matches   70;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     242 NRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITE 301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     242 NRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITE 301

Qy     302 DLGLELKDAT 311
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Db     302 DLGLELKDAT 311


RESULT 3
B86674
60 KD chaperonin [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: B86674
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86674
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <STO>
A;Cross-references: GB:AE005176; PID:g12723267; PIDN:AAK04492.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL

  Query Match            10.3%;  Score 56;  DB 2;  Length 542;
  Best Local Similarity  100.0%;  Pred. No. 5e-47;
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Qy      44 GSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIV 99
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RESULT 4
AD1333
class I heat-shock protein (chaperonin) GroEL [imported] - Listeria monocytogenes (strai
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AD1333
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00146.1; PID:g16411538; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL

  Query Match            5.7%;  Score 31;  DB 2;  Length 542;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-22;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels

Qy     266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296
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Db     266 RGTFNVVAVKAPGFGDRRKAMLEDIAILTGG 296


RESULT 5
B36917
heat shock protein GroEL - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C;Accession: B36917
R;Segal, G.; Ron, E.Z.
J. Bacteriol. 175, 3083-3088, 1993
A;Title: Heat shock transcription of the groESL operon of Agrobacterium tumefaciens
A;Reference number: A36917; MUID:93259955; PMID:8098329
A;Accession: B36917
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <SEG>
A;Note: sequence extracted from NCBI backbone (NCBIN:131959, NCBIP:131961)
C;Superfamily: chaperonin groEL

  Query Match            5.0%;  Score 27;  DB 2;  Length 544;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-18;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
           |||||||||||||||||||||||||||
Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301


RESULT 6
S23918
groEL protein - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S23918
R;Segal, G.; Ron, E.Z.
submitted to the EMBL Data Library, August 1992
A;Description: Cloning and sequencing of the GroE operon of Agrobacterium tumefacie
A;Reference number: S23917
A;Accession: S23918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <SEG>
A;Cross-references: EMBL:X68263; NID:g1019913; PIDN:CAA48331.1; PID:g39095
C;Superfamily: chaperonin groEL

  Query Match            5.0%;  Score 27;  DB 2;  Length 544;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-18;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
           |||||||||||||||||||||||||||
Db     275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301


RESULT 7
B97442
60K chaperonin (protein cpn60) (groEL protein) [imported] - Agrobacterium tumefacie
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: B97442
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.;
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; La
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology
A;Reference number: A97359; PMID:11743194
A;Accession: B97442
A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-544 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86491.1; PID:g15155641; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_1220
A;Map position: circular chromosome
C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 8
AD2660
60 KDA chaperonin [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C;Accession: AD2660
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AD2660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-544 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41698.1; PID:g17739044; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: groEL
A;Map position: circular chromosome
C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 9
JN0509
heat shock protein groEL (clone Rhz A) - Rhizobium meliloti
N;Alternate names: chaperonin groEL protein
C;Species: Rhizobium meliloti
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: JN0509
R;Rusanganwa, E.; Gupta, R.S.
Gene 126, 67-75, 1993
A;Title: Cloning and characterization of multiple groEL chaperonin-encoding genes in Rhi
A;Reference number: JN0509; MUID:93231539; PMID:8097179
A;Accession: JN0509
A;Molecule type: DNA
A;Residues: 1-545 <RUS>
A;Cross-references: GB:M94192; NID:g152233; PIDN:AAA26285.1; PID:g152235
C;Comment: This protein plays a role in protein folding and in the extracellular transpo
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 5.0%; Score 27; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 10
S47530
chaperonin groEL - Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S47530
R;Hotokezaka, H.; Hayashida, H.; Ohara, N.; Nomaguchi, H.; Kobayashi, K.; Yamada, T.
Biochim. Biophys. Acta 1219, 175-178, 1994
A;Title: Cloning and sequencing of the groESL homologue from Porphyromonas gingivali
A;Reference number: S47530; MUID:94368851; PMID:8086460
A;Accession: S47530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <HOT>
A;Cross-references: EMBL:D17342; NID:g532498; PIDN:BAA04161.1; PID:g532499
A;Note: the source is designated as Bacteroides gingivalis
C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 11
C95311
groEL2 chaperonin [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSym
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: C95311
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.;
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh,
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium mel
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95311
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65053.1; PID:g14523485; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hub
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: groEL2
A;Genome: plasmid
C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 3:7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 12
I40331
Cpn60 protein (GroEL) - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 26-Aug-1999
C;Accession: I40331
R;Fernandez, R.C.; Weiss, A.A.
Gene 158, 151-152, 1995
A;Title: Cloning and sequencing of the Bordetella pertussis cpn10/cpn60 (groESL) homolog
A;Reference number: I40330; MUID:95309719; PMID:7789805
A;Accession: I40331
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-547 <RES>
A;Cross-references: EMBL:U12277; NID:g968918; PIDN:AAA74967.1; PID:g968920
C;Genetics:
A;Gene: cpn60
C;Superfamily: chaperonin groEL

Query Match 5.0%; Score 27; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 3.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTVI 299
||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTVI 301

RESULT 13
C89994
GroEL protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89994
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89994
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-538 <KUR>
A;Cross-references: GB:BA000018; PID:g13701823; PIDN:BAB43116.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL

Query Match 4.8%; Score 26; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 SDFDREKLQERLAKLAGGVAVIKVGA 381
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Db 356 SDFDREKLQERLAKLAGGVAVIKVGA 381

RESULT 14
JN0601
heat shock protein 60 - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
C;Accession: JN0601; PN0508
R;Ohta, T.; Honda, K.; Kuroda, M.; Saito, K.; Hayashi, H.
Biochem. Biophys. Res. Commun. 193, 730-737, 1993
A;Title: Molecular characterization of the gene operon of heat shock proteins HSP60 and
A;Reference number: JN0600; MUID:93290669; PMID:7916607
A;Accession: JN0601
A;Molecule type: DNA
A;Residues: 1-539 <OH1>
A;Accession: PN0508
A;Molecule type: protein
A;Residues: 1-21 <OH2>
C;Genetics:
A;Gene: hsp60
C;Superfamily: chaperonin groEL
C;Keywords: heat shock; stress-induced protein

Query Match 4.8%; Score 26; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 SDFDREKLQERLAKLAGGVAVIKVGA 381
||||||||||||||||||||||||||
Db 357 SDFDREKLQERLAKLAGGVAVIKVGA 382

RESULT 15
JN0512
heat shock protein groEL (clone Rhz C) - Rhizobium meliloti
N;Alternate names: chaperonin groEL protein
C;Species: Rhizobium meliloti
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C;Accession: JN0512
R;Rusanganwa, E.; Gupta, R.S.
Gene 126, 67-75, 1993
A;Title: Cloning and characterization of multiple groEL chaperonin-encoding genes i
A;Reference number: JN0509; MUID:93231539; PMID:8097179
A;Accession: JN0512
A;Molecule type: DNA
A;Residues: 1-541 <RUS>
A;Cross-references: GB:M94191; NID:g152236; PIDN:AAA26287.1; PID:g152238
C;Comment: This protein plays a role in protein folding and in the extracellular tr
C;Genetics:
A;Gene: groEL
C;Superfamily: chaperonin groEL
C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 4.8%; Score 26; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 273 AVKAPGFGDRRKAMLEDIAILTGGTV 298
||||||||||||||||||||||||||
Db 275 AVKAPGFGDRRKAMLEDIAILTGGTV 300

Search completed: April 8, 2003, 14:38:14
Job time : 50 secs